



Relevance of nuclear receptor expression in a T_hreg cell line, HOZOT: RXR α and PPAR γ negatively regulate IFN- γ production

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ABSTRACT

Nuclear receptors (NRs) have recently received much attention for their newly discovered roles in T cell development, as exemplified by RAR α (Treg cells) and ROR γ t (Th17 cells). In previous studies, we characterized a new type of T cell subset, designated as T_hreg (cytotoxic, helper, and regulatory T) cells, in terms of its cytokine signature. In this study, we investigated the expression and functional relevance of NRs in T_hreg cells by performing mRNA profiling of HOZOT, a cord blood-derived T_hreg cell line. We identified eleven inducible and eight constitutively expressed NRs in HOZOT. Among these NRs, RXR α and PPAR γ showed features of signature NRs of T_hreg cells because they were selectively expressed in HOZOT compared with other T cell subsets. These NRs exhibited contrasting expression patterns, as RXR α was independent of anti-CD3/28 antibody stimulation while PPAR γ was stimulated-dependent. Upon agonist treatment, both proteins translocated to the nucleus and inhibited IFN- γ production through binding to the promoter region of the IFN- γ gene. These results provide new insight into the roles of RXR α and PPAR γ in T cell biology, especially in their biological relevance in T_hreg cells.

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1. Introduction

Nuclear receptors (NRs) are ligand-activated transcription factors that modulate gene expression through binding to specific hormone response elements. A total of forty-eight human NRs have been identified and classified into seven groups: the thyroid hormone receptor family, the retinoid X receptor family, the estrogen receptor family, the neuron growth factor IB family, the steroid family, the germ cell nuclear factor, and others [1]. Since NRs function as transcription factors, their roles include diverse physiological and pathological processes such as cellular development and differentiation, metabolic homeostasis, cancer, autoimmune diseases, inflammatory diseases, and diabetes [2,3].

Studies of NRs have recently focused on T cell biology. Naïve CD4⁺ T cells differentiate into distinct types of T cells under the appropriate inducing conditions. Among them, T helper (Th) 17, a subset of T helper cells characterized by secretion of Interleukin (IL)-17, have been associated with the pathogenesis of autoimmunity [4–6] and their development was linked to the expression of retinoic acid-related orphan receptor (ROR) γ t [7]. Under Th17 differentiation conditions, IL-6 and transforming growth factor (TGF)- β induce

the expression of ROR γ t, which directly or indirectly promotes IL-17 transcription. However, it is not yet known whether this process is ligand-dependent. Regulatory T (Treg) cells are another example of NR-controlled T cells. Forkhead-winged helix family transcription factor 3⁺ Treg cells are induced in a manner reciprocal to Th17 cells by IL-2 and TGF- β , and a retinoic acid receptor (RAR) ligand such as retinoic acid can enhance their differentiation [8]. Tr1 cells (an IL-10-producing type of Treg cell), are induced by an active form of vitamin D3 [9]. Interestingly, retinoic acid promotes Treg cell differentiation in the intestine whereas vitamin D3 does the same in the skin, highlighting specialized roles for nuclear receptor ligands in local tissues.

In previous studies, we described a new and distinct type of Treg cell line, termed HOZOT [10]. HOZOT exhibited multifunctional properties such as suppression of mixed lymphocyte reaction (MLR), helper activity under anti-CD3 stimulation conditions, cytotoxic activity and cell-in-cell activity against human tumor cells [10–13]. Therefore, we designated these cells as T_hreg (cytotoxic, helper, and regulatory) cells. By mRNA profiling, cytokines and chemokines such as IFN- γ , IL-10, RANTES, and IL-8 were identified as signature molecules of T_hreg cells [14,15]. We also reported the low expression of micro RNA (miR)-155 as a characteristic of T_hreg cells, in contrast to the high miR-155 expression levels observed in natural Treg cells [16]. Since NRs play important roles in T cell development and function, we focused this study on the biological relevance of NR

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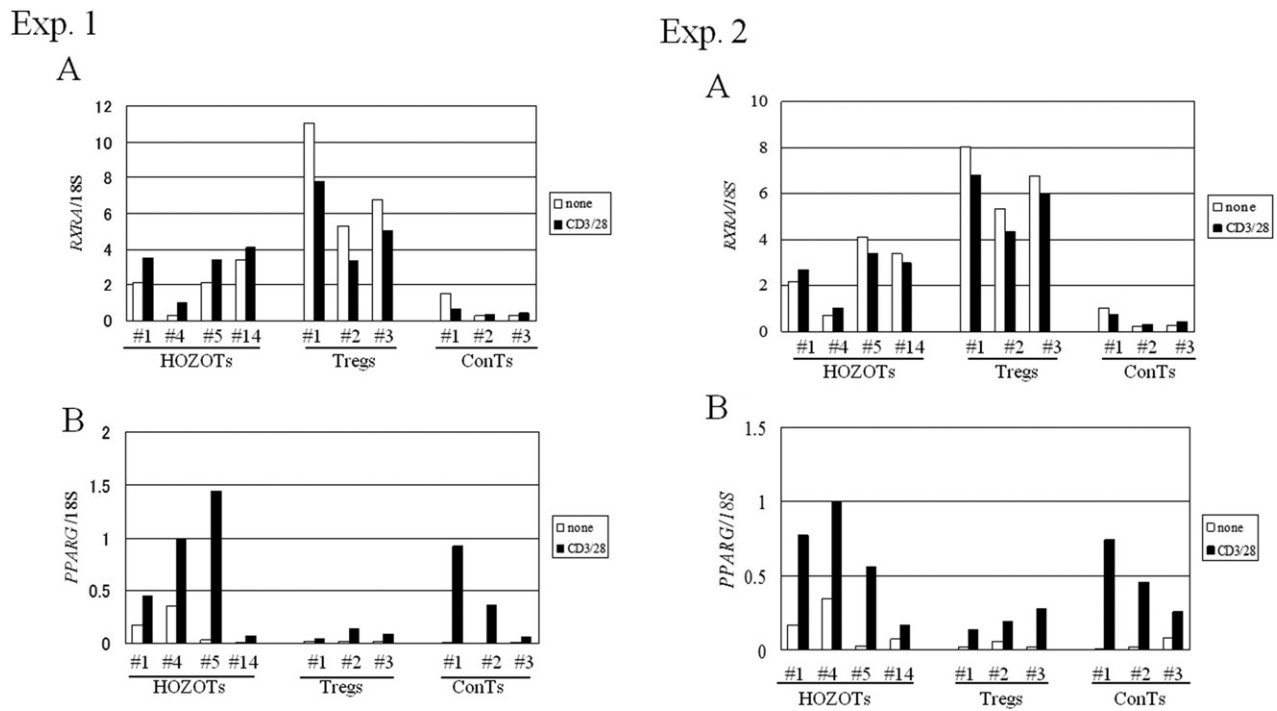


Fig. 1. *RXRA* and *PPARG* were defined as signature NRs by comparing their expression in HOZOTs to those in other T cell subsets. Expression of *RXRA* (A) or *PPARG* (B) mRNA in T cell subsets is shown as a ratio of *RXRA* or *PPARG* mRNA to 18S rRNA, respectively. RNA was harvested after 24 h culture with or without anti-CD3/28 antibody stimulation, and the relative amount of mRNA was measured by RT-qPCR. All values were standardized by defining the sample value of the anti-CD3/28 antibody stimulated HOZOT (#4) as 1.0. Results of two independent experiments are presented as experiment 1 (left) and 2 (right).

expression and function in Treg cells. To accomplish this, we first examined mRNA expression of NRs in HOZOT using DNA microarray analysis and identified retinoid X receptor α (RXR α) and peroxisome proliferator-activated receptor (PPAR) γ as signature NRs. We further investigated the effects of agonistic ligands of these NRs on protein localization and cytokine production.

2. Materials and methods

2.1. Reagents

Interleukin (IL)-2 was purchased from Pepro Tech EC Ltd. (London, UK). Anti-CD3 ϵ (UCHT-1), anti-CD28 (37407) antibodies, and RANTES ELISA kits were purchased from R&D Systems (Minneapolis, MN, USA). IL-10 ELISA kits were purchased from eBioscience (San Diego, CA, USA). IFN- γ ELISA kit was obtained from Hayashibara Biochemical Labs. (Okayama, Japan). Anti-PPAR γ (E-8), either Alexa 488-conjugated or unconjugated, and anti-human RXR α (D-20) antibodies were purchased from Santa Cruz Biosciences (Santa Cruz, CA, USA). Ligands for NRs were obtained as follows: thiazolidinedione (TZD) and GW9662 were purchased from WAKO chemical (Osaka, Japan) and Calbiochem (San Diego, CA), respectively. Net-3IP (RXR specific agonist) and NS-4TF (RXR antagonist) were synthesized as described in the previous reports [17–19].

2.2. Generation of HOZOT cells

The generation of HOZOT cell lines was described in detail previously [10]. Briefly, umbilical cord blood (UCB) samples were collected at Kurashiki Medical Center after obtaining informed consent according to the Declaration of Helsinki. Mononuclear cells (MNC) derived from UCB were enriched using Ficoll-paque density centrifugation and co-cultured with mouse stromal cell lines, ST2 or MS-5, in RPMI-1640 medium containing 10% fetal bovine serum (FBS). Two to three weeks later, proliferative cells, which exhibited cytotoxicity against

the stromal cell line, were expanded in the presence of IL-2 (10 ng/mL). The expanded cells, termed HOZOT, were used for further analysis.

2.3. Cell preparation

The preparation of conventional T (ConT) cells and naturally occurring T regulatory (nTreg) cells was described previously. UCB-derived CD25 $^{+}$ cells were isolated by positive selection with directly conjugated anti-CD25 magnetic beads (Miltenyi Biotech, Bergisch Gladbach, Germany). The purity of CD25 $^{+}$ cells were >90%. CD25 $^{+}$ T cells were used for the preparation of nTreg cells. CD25 $^{-}$ cells were treated with anti-CD4 magnetic beads (Miltenyi Biotech), and CD4 $^{+}$ cells were enriched using the Midi-MACS system. The purity of CD4 $^{+}$ CD25 $^{-}$ cells were >95%. CD4 $^{+}$ CD25 $^{-}$ T cells were used for the preparation of ConT cells. CD25 $^{+}$ T cells and CD4 $^{+}$ CD25 $^{-}$ T cells were stimulated on plates coated with anti-CD3/CD28 antibodies in RPMI-1640 medium containing 10% FBS at 37°C in 5% CO $_2$ in the presence of 10 ng/mL IL-2. Growing cells were used as nTreg and ConT cells.

2.4. DNA microarray analysis

Preparation of DNA microarray samples was described previously [15]. Total RNA from HOZOT was isolated with RNeasy kit (Qiagen, Valencia, USA) according to the manufacturer's instructions. The samples were processed and analyzed at the Bio Matrix Research Institute (Nagareyama, Chiba, Japan) using U133 Plus 2.0 Affymetrix Gene Chip arrays containing 54,675 human genes and transcripts. DNA microarray data of HOZOT were normalized and analyzed by Gene Spring GX software (Agilent Technologies, Wilmington, DE, USA).

2.5. Real-time quantitative polymerase chain reaction (RT-qPCR)

The expression of NRs was analyzed at the mRNA level by RT-qPCR. Total RNA was isolated from HOZOT, ConT cells, nTreg cells and CD4 $^{+}$ CD25 $^{-}$ T cells using RNeasy kit (Qiagen). RT-qPCR was done as

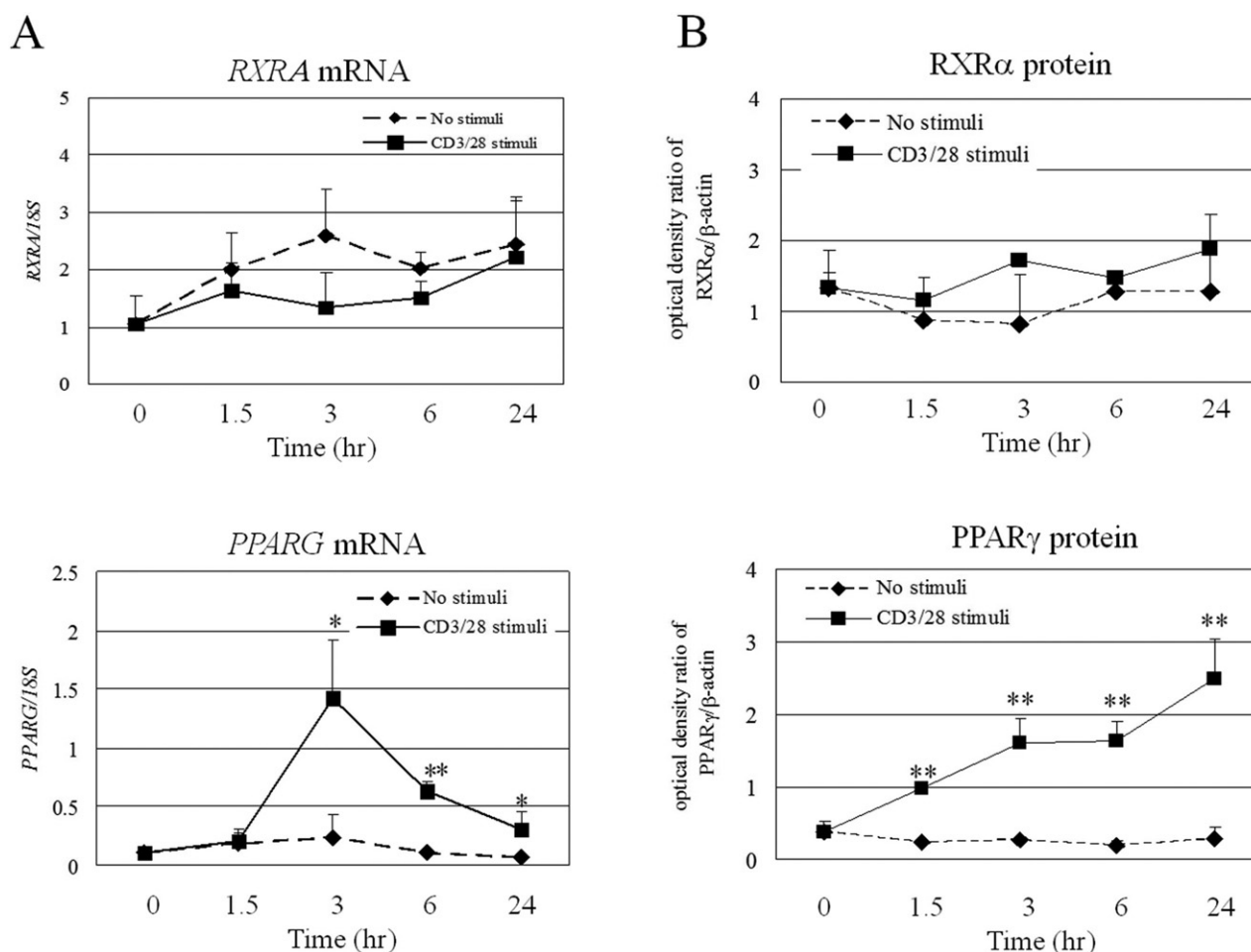


Fig. 2. Time course study showed *RXRA* as a constitutively expressed gene and *PPARG* as an inducible gene. (A) The time course of *RXRA* or *PPARG* mRNA expression by HOZOT cells was analyzed. The amount of *RXRA* or *PPARG* mRNA in 0, 1.5, 3, 6, and 24 h culture samples was measured by RT-qPCR. The ratios of *RXRA* or *PPARG* mRNA to 18S rRNA are shown after standardization as in Fig. 1. (B) The time course of *RXRα* or *PPARγ* protein expression was studied. *RXRα* or *PPARγ* protein in 0, 1.5, 3, 6, and 24 h culture samples was detected by Western blotting using anti-*RXRα* or anti-*PPARγ* antibody. After stripping, the membrane was reprobed with anti- β -actin antibody. The optical density ratios of *RXRα* or *PPARγ* bands relative to a corresponding β -actin band are shown for quantitative analysis. The values are shown as the means \pm SD of three experiments. * and **: $p < 0.05$ and $p < 0.01$ compared with the values of the control without antibody stimulation, respectively.

described previously [15]. The primer sequences used in this study are described elsewhere (Suppl. Fig. 1).

2.6. Immunohistochemistry

Cells were cytospun onto slide glasses and fixed with ice-cold methanol for 2 min. After treatment with blocking buffer containing 1% FBS in PBS, *RXRα* proteins were stained using an anti-*RXRα* antibody and Alexa 488-conjugated anti-rabbit IgG antibody, and *PPARγ* was stained with Alexa 488-conjugated anti-*PPARγ* antibody. The nuclei were counterstained with 0.5 μ g/mL Hoechst 33258 in PBS.

2.7. Western blotting analysis

Western blotting was performed as previously described [20]. Briefly, equivalent amounts of total protein were loaded onto 10% SDS polyacrylamide gels. After electrophoresis, proteins were electrotransferred onto the nitrocellulose membranes and reacted with the appropriate primary antibody according to standard methods. Bound immunocomplexes were visualized by use of Super Signal West Pico (Pierce, Rockford, IL). In some experiments, the membranes were stripped and then reprobed with anti-acetyl histone H3 antibody (Millipore International, Inc., Temecula, CA) or anti- β -actin antibody to confirm the equality of total nuclear or cytoplasmic protein loading.

2.8. Cytokine production assays

Six-well flat-bottom plates were precoated with anti-CD3 (1 μ g/mL) and anti-CD28 (1 μ g/mL) antibodies. HOZOT cells were cultured in the six-well flat-bottom plates at 1×10^6 /well/mL for 16 h, in RPMI-1640 medium containing 10% FBS and 10 ng/mL IL-2. HOZOT cells were collected and washed with RPMI-1640 medium containing 10% FBS and resuspended in the same medium. HOZOT cells were cultured in 24-well flat-bottom plates, which were coated with anti-CD3/CD28 (1 μ g/mL) antibody at 5×10^5 /well for one day with or without increasing concentrations of TZD, Net-3IP, GW9662, and NS-4TF, each alone or in combination. Cell culture supernatants were harvested and analyzed for IFN- γ , RANTES and IL-10 production using ELISA kits.

2.9. Chromatin immunoprecipitation (ChIP) assays

Chromatin immunoprecipitation was performed as previously described [14]. Briefly, HOZOT cells were fixed with 1% formaldehyde for 10 min at room temperature, and then the fixation was stopped with 1.25 M glycine. Fixed cells were washed with cold PBS. Cells were treated with lysis buffer (Santa Cruz Biotechnology) and sonicated six times (10 s each) to prepare chromatin extracts. Protein G beads (100 μ L) were incubated with anti-*PPARγ* antibody (5 μ g), anti-*RXRα* antibody (5 μ g), control mouse IgG (5 μ g), or control rabbit

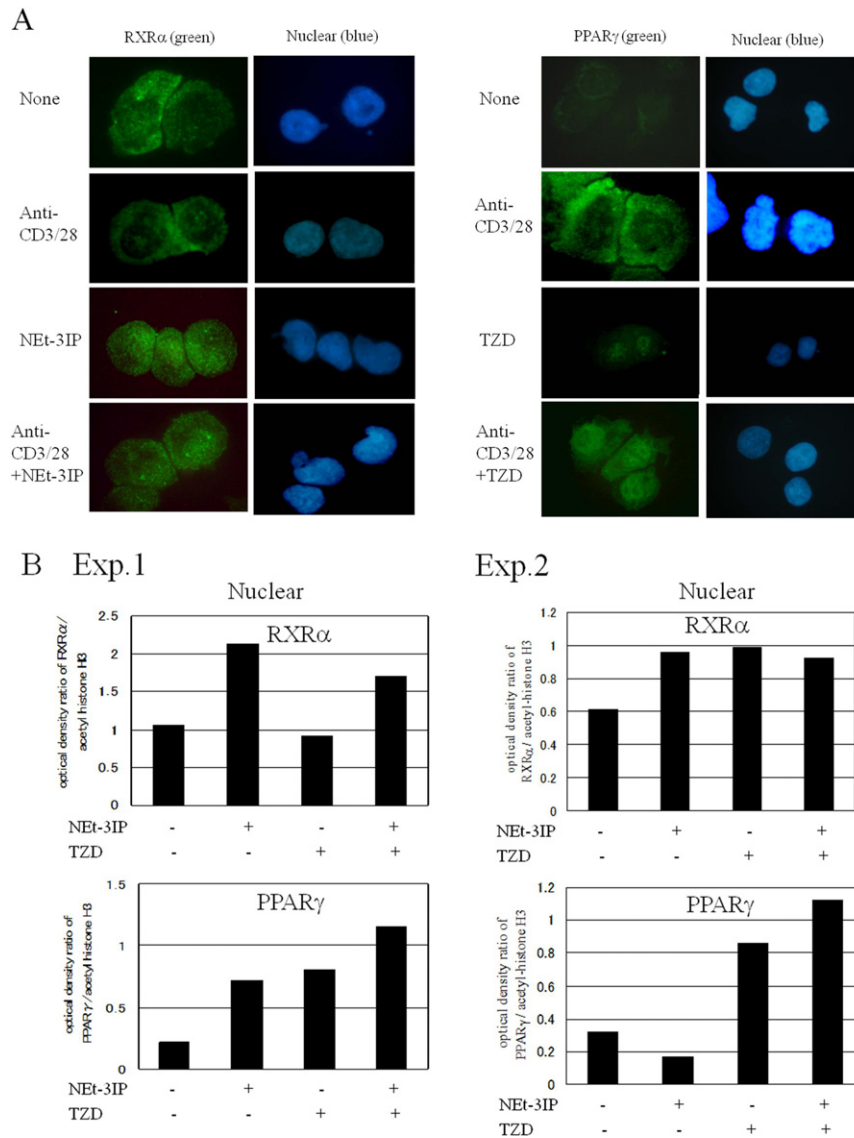


Fig. 3. Cellular localization of RXR α or PPAR γ protein analyzed by immunohistochemistry and Western blotting. (A) HOZOT cells were stimulated with 1 μ g/mL of anti-CD3/28 antibody for 16 h and then treated with 1 μ M TZD or NET-3IP for 3 h. For immunohistochemistry, cells were stained with rabbit anti-RXR α antibody (green) or mouse anti-PPAR γ antibody (green) and counterstained with Hoechst 33258 (blue). (B) HOZOT cells were stimulated with 1 μ g/mL anti-CD3/28 antibody for 16 h and then treated with 1 μ M TZD and/or NET-3IP for 3 h. Nuclear fraction was prepared and the subcellular localization of RXR α or PPAR γ was determined by Western blotting. After stripping, the membrane was reprobed with anti-acetyl-Histone H3 antibody. The optical density ratios of RXR α or PPAR γ bands relative to corresponding acetyl-Histone H3 bands are shown for quantitative analysis. Results of two independent experiments are presented as experiment 1 (left) and 2 (right). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

IgG (5 μ g) at 4 °C overnight. Protein G beads were washed three times with cold PBS and then chromatin extracts were incubated with Protein G beads at 4 °C overnight. After washing the immunoprecipitates with washing buffer (Santa Cruz Biotechnology), DNA was eluted by incubation with extraction buffer (Santa Cruz Biotechnology) at 67 °C overnight. The DNA samples were purified and used as templates for RT-qPCR. Bioinformatic analysis was performed using rVISTA. The PPAR γ response element (PPRE) of the double repeat (DR)1-type was located in the IFN- γ promoter region at 493 bp upstream of the IFN-G transcription start site.

2.10. Statistical analysis

Statistical analysis was performed by one-way ANOVA, followed by LSD post hoc test, with an acceptable significance probability level at <0.01 or <0.05.

3. Results

3.1. Expression profiles of NRs in HOZOT

In our previous studies, we characterized HOZOT by defining the cells' cytokine signature [15] and found that two chemokines, RANTES and IL-8, were produced at high levels by HOZOT.

To further analyze signature molecules, we focused on NR expression in HOZOT by comparing three conditions: unstimulated, ST2-stimulated, and anti-CD3/CD28 antibody-stimulated. The results of DNA microarray analysis are summarized in Table 1. We found that 19 NRs (RARA, PPARG, PPARG, PPARG, REV-ERBA, REV-ERBA, RORA, RORG, LXR, RXRA, RXRB, TR2, TR4, ERRA, GR, NGFIB, NURR1, and NOR1) were expressed in HOZOT-4 among a total of human 48 NRs. All of the expressed genes were categorized into two groups, either inducible or constitutively expressed genes (Table 1). The inducible genes, the expression of which was increased two- to 3347-fold by

Table 1

Nineteen nuclear receptors expressed in HOZOT were detected by DNA microarray analysis.

Common name	Symbol	Genbank	Fold change			Raw data			Flags			
			(-)	ST2	CD3/28	(-)	ST2	CD3/28	(-)	ST2	CD3/28	
Inducible												
	RARA	NR1B1	AV657604	1	1.7	2.1	13.0	23.0	37.6	P	P	P
	PPARG	NR1C3	AK027107	1	2.3	15.9	7.1	17.0	155.8	A	P	P
	REV-ERBAA	NR1D1	X72631	1	2.6	12.9	9.7	26.6	172.2	A	A	P
	REV-ERBAB	NR1D2	AI761621	1	0.7	3.3	43.4	34.0	195.6	P	P	P
	RORG	NR1F3	AI218580	1	0.9	11.7	3.3	3.2	51.7	A	A	P
	VDR	NR1I1	AA772285	1	2.1	8.2	132.5	296.1	1504.2	P	P	P
	ERRA	NR3B1	L38487	1	1.3	2.0	71.3	95.7	196.5	P	P	P
	GR	NR3C1	AI432196	1	0.9	2.2	489.4	471.5	1501.1	P	P	P
	NGFIB	NR4A1	NM.002135	1	3.9	112.3	5.4	22.5	837.0	A	P	P
	NURR1	NR4A2	NM.006186	1	2.6	247.3	11.3	30.9	3856.6	A	P	P
	NOR1	NR4A3	U12767	1	1.5	3346.8	0.8	1.3	3693.9	A	A	P
Constitutive												
	LXRB	NR1H2	NM.007121	1	1.1	1.7	76.3	88.4	175.9	P	P	P
	PPARA	NR1C1	AF086231	1	1.7	1.4	11.5	20.2	22.9	P	P	P
	PPARB	NR1C2	BC002715	1	1.0	0.9	17.2	18.2	20.3	P	P	M
	RORA	NR1F1	AK025371	1	0.8	0.4	31.7	25.9	17.6	P	P	P
	RXRA	NR2B1	NM.002957	1	1.3	0.7	53.6	71.2	55.3	P	P	P
	RXRB	NR2B2	BC001167	1	0.7	0.9	105.3	80.1	136.7	P	P	P
	TR2	NR2C1	NM.003297	1	0.9	0.6	113.1	112.1	100.2	P	P	P
	TR4	NR2C2	AL138444	1	1.1	0.5	346.3	394.2	228.9	P	P	P

anti-CD3/CD28 stimulation, included *RARA*, *PPARG*, *REV-ERBAA*, *REV-ERBAB*, *RORG*, *VDR*, *ERRA*, *GR*, *NGFIB*, *NURR1*, and *NOR1*. The constitutively expressed genes, the expression levels of which were less than two-fold even after antibody stimulation, included *LXRB*, *PPARA*, *PPARB*, *RORA*, *RXRA*, *RXRB*, *TR2*, and *TR4*.

3.2. High expression of *RXRA* and *PPARG* as candidate HOZOT markers

Next, we compared the expression of the NRs listed in Table 1 among different T cell subsets (HOZOT, nTreg cells, ConT cells, and naïve T cells) using RT-qPCR. HOZOT preferentially expressed five NRs: *PPARG*, *NGFIB*, *NURR1*, *NOR1*, and *RXRA* (data not shown). To validate the expression profiles of these NRs, we examined their expression by RT-qPCR using four sets of HOZOTs and three sets each of ConT and nTreg cells. *RXRA* mRNA was highly expressed in three of the four sets of HOZOTs and all three sets of Tregs cell lines compared to the three sets of ConT cell lines, whereas the mRNA levels of *PPARG* in HOZOTs (except for #14) and ConT cells (except for #3) was higher than in Tregs (Fig. 1). On the other hand, the expression levels of *NGFIB*, *NURR1*, and *NOR1* mRNA varied widely even among the four sets of HOZOTs (data not shown). Therefore, we focused our interests on *RXRA* and *PPARG* to explore the relevance of these NRs in HOZOT's characterization.

3.3. Time course of mRNA and protein expression of *RXRA* and *PPARG* in HOZOT

As shown above, *RXRA* was constitutively expressed while *PPARG* was inducible. Time course studies revealed in detail the cells' expression at both mRNA and protein levels. Unstimulated HOZOT cells expressed significant levels of *RXRα* mRNA and protein, whereas they expressed low levels of *PPARγ* mRNA and protein (Fig. 2A and B). Even after anti-CD3/CD28 antibody stimulation, *RXRα* expression did not change much between 1.5 and 24 h. In contrast, *PPARγ* expression increased after antibody stimulation and reached a maximum after 3 h (Fig. 2A). *PPARγ* protein expression increased steadily upto 24 h after antibody stimulation (Fig. 2B). We confirmed these properties by flow cytometric analysis (data not shown).

3.4. Subcellular localization of *RXRα* and *PPARγ* in HOZOT cells

To examine the subcellular localization of *RXRα* and *PPARγ* proteins in HOZOT cells, we performed immunohistochemical analysis and Western blotting analysis using nuclear extracts. *RXRα* protein was detected in the cytoplasm under both anti-CD3/28 antibody stimulated and unstimulated conditions. On the other hand, *PPARγ* protein was weakly detected under unstimulated conditions, but upon Ab stimulation, it appeared in the cytoplasm at high levels. When treated with agonistic ligands for *RXRα* and *PPARγ*, NEt-3IP and TZD, respectively, both *RXRα* and *PPARγ* proteins were translocated to the nuclei (Fig. 3A). NEt-3IP is an agonist specific for *RXRα/β* but not

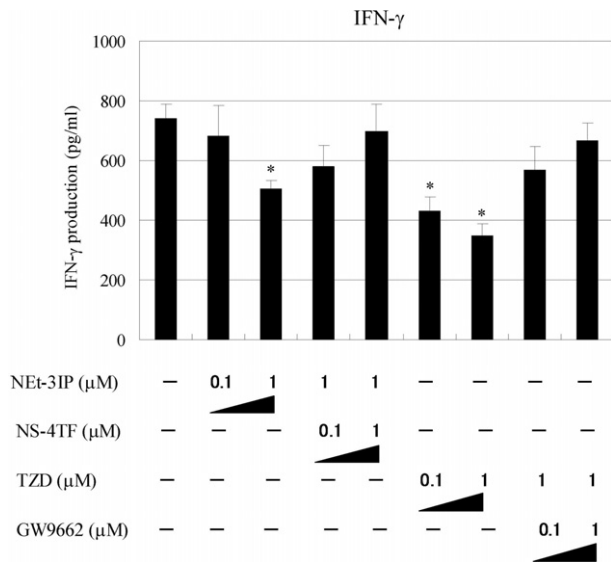


Fig. 4. The suppressive effects of agonists or antagonists of RXR α or PPAR γ on IFN- γ production by HOZOT cells. IFN- γ production was measured by stimulating HOZOT cells with 1 μ g/mL anti-CD3/28 antibody for 16 h. For the agonist and antagonist treatment, HOZOT cells were pretreated for 30 min with 0.1 and 1 μ M NS-4TF (RXR α antagonist) or GW9662 (PPAR γ antagonist) and then treated with 0.1 and 1 μ M NEt-3IP or TZD. Culture supernatants were collected for determining IFN- γ levels by ELISA. The values are shown as the means \pm SD. Data are representative results of at least two independent experiments. * $p < 0.01$ compared with the values of the control without ligand stimulation.

RXR γ , whereas TZD is specific for PPAR γ but not PPAR α/β . Western blotting analysis confirmed the localization of both NRs (Fig. 3B).

3.5. NEt-3IP and TZD inhibit IFN- γ production by HOZOT cells

To further investigate the functional relevance of RXR α and PPAR γ proteins in HOZOT cells, we treated HOZOT cells with their agonistic ligands and observed the effects on cytokine productions. HOZOT cells produce high amounts of IFN- γ , RANTES, and IL-10. Among them, IFN- γ production was inhibited in a dose-dependent manner by either NEt-3IP or TZD treatment alone (Fig. 4). To examine antagonist effects, we next treated HOZOT cells with combinations of agonists and antagonists, namely RXR α agonist (NEt-3IP) plus antagonist (NS-4TF) or PPAR γ agonist (TZD) plus antagonist (GW9662). Each antagonist abolished its corresponding agonist's effects on IFN- γ production (Fig. 4). In contrast, no significant decrease or increase in RANTES and IL-10 production was observed by NEt-3IP and TZD treatment (Suppl. Fig. 2). Cell viability was maintained at high levels at concentrations up to 10 mM for both ligands (data not shown). These results indicated that both NRs were functionally involved in IFN- γ production in HOZOT cells.

3.6. PPAR γ and RXR α directly bind to the IFN- γ gene

To explain the mechanism of suppression of IFN- γ production by NEt-3IP and TZD in HOZOT cells, we hypothesized that RXR α and PPAR γ could directly bind to the IFN- γ promoter region. We first performed a bioinformatics search for DR1 and PPRE sites, specific binding sequences for nuclear receptors, on the IFN- γ promoter region using web-based software, rVISTA. A DR1-type PPRE was found in the IFN- γ promoter region at 493 bp upstream of the IFN- γ transcription start site (Fig. 5). We next performed a ChIP analysis with anti-RXR α antibody and anti-PPAR γ antibody using HOZOT cells treated with NEt-3IP or TZD. As shown in Fig. 6, low amounts of RXR α and PPAR γ proteins were bound to the IFN- γ promoter region, even in ligand-unstimulated HOZOT cells. Upon ligand stimulation, increased

Human IFN- γ promoter region

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ACAGGTGTGAGCCACTGCGTCTGGAACCTCCCTGGGAATATCTCTACACTGTATTTCAAGGAITTA
ATATGACAAAAAGAAATGTCAAATACCTTATTAACAATGTAGTATTTGATGACATACTGAAGTACTATT
TGGGATATATTTGTTTAAATACAATATATTTTAAATATATTTACCTTTTAAAAAACTTTTATTAAT
GAGGTACTAGATCAITTAATTAATTAACCTGTGTGGCTGTATTGTATTCTACTGGGCAGTGCTGATCTAG
AGCAATTGAAACTGTGGTAGATATTTTAACTAACTCACTGATGAGGACTTCTCACCAGATTTG
TTCTTTTAAACCGCATCTTCTCTGCTTCTGGTCAITTTGCAAGAAAAATTTAAAGGCTGCCCTTTG
TAAAGGTTTGAGAGGCTTGAATTTTACCTGTTTCCCAACCAAGCAAGCAATGATCAATGTGCT
TTGTGAATGAAGAGTCAACATTTTACAGGGCGAAGTGGGGAGGTACAAAAATTTCCAGTCTTGA
ATGGTGTGAAGTAAAGTGCTTCAAAGAATCCACAGAGATGGCAGGTGGGCATAATGGGTCTGT
CTCATGTCACAAAGACCAAGGAGTCTAAAGGAACTCTAATCAACACCCAAATGCCACAAACC
TTAGTTATTAATACAACTATCATCTCTGCTATCTGTCACCATCTCATCTTAAATAAATTTGTGAAAT
ACGTAATCTCAGGAGACTTCAATTAGGTATAATACAGCAGCCAGAGGAGTGCAGCAGTCTTCT
GATCATCTGAAGTACAGCTATTAGAAGAGAAAGTACAGTTAAGTCTTGGACCT

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Fig. 5. Bioinformatics analysis of the PPRE/DR-1 region in the IFN- γ promoter region. The sequence of the IFN- γ promoter region from – 810 bp to 0 bp. The PPRE/DR-1 sequence is underlined and marked red. Primers used for ChIP-qPCR are marked with black arrows. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

amounts of RXR α and PPAR γ proteins were detected in ChIP samples with specific antibodies but not in those with control antibodies. These results supported our hypothesis that the inhibitory effects of RXR α and PPAR γ agonists on IFN- γ production operated through the direct binding of these agonists to the IFN- γ promoter.

4. Discussion

Expression profiles of NRs during cell development and differentiation have been reported by a number of investigators. For example, Xie et al. [21] reported that ERR β , DAX-1 and LRH-1 controlled the development of embryonic stem cells. According to Barish et al. [22] 28 NRs including RXR α and PPAR γ are involved in the activation of macrophages. A number of NRs control T cell differentiation, for example ROR γ t serving as a specific marker of Th17 cells. Thus, comprehensive analysis of NR expression in a new type of T cell, HOZOT, was a necessary and interesting step to enhance our understanding of this cell line. In this study, we found that 19 of 48 NRs were expressed in HOZOT, and identified eight genes (RXRA and TR2, etc.) that were constitutively expressed, and 11 genes (NGFIB, NOR1, NURR1 and PPARG, etc) that were inducible. Among them, RXRA and PPARG were selected for further analyses due to their more selective expression patterns compared with other T cell subsets.

HOZOTs expressed both NRs at relatively high levels, whereas Tregs showed the highest and the lowest expression of RXR α and PPAR γ , respectively. It is intriguing that the two NR expression patterns were identified in T cell subsets, suggesting distinct functional roles for these NRs in T cell biology. RXR α functions as a transcription factor by forming a heterodimer complex with other NRs such as PPAR γ , VDR, LXR β , RAR α , and NURR1. Therefore, RXR α availability determines the function of these NRs. It is noteworthy that the expression of RXR α remained unchanged after ST2 or T cell receptor stimulation whereas the expression of PPAR γ , VDR, RAR α , and NURR1 was increased by stimulation. Given the fact that T-lymphocyte proliferation and survival were diminished by RXR α disruption [23] and that the anti-apoptotic gene Bcl2a1 was up-regulated by RXR α agonist treatment [24], RXR α may play a central role by balancing the availability for heterodimer formation with other NR partners. In this regard, it will be interesting to elucidate how HOZOTs control heterodimer complex formation.

Since the *in vivo* counterpart of HOZOTs has not yet been identified, the physiological relevance of high-level expression of RXR α and PPAR γ remains unclear. In general, RXR plays important regulatory roles in metabolic disorders, such as type 2 diabetes, hyperlipidemia, and atherosclerosis [25,26] and also in the control of innate inflammatory responses [27]. PPAR γ possesses a broad range of biological

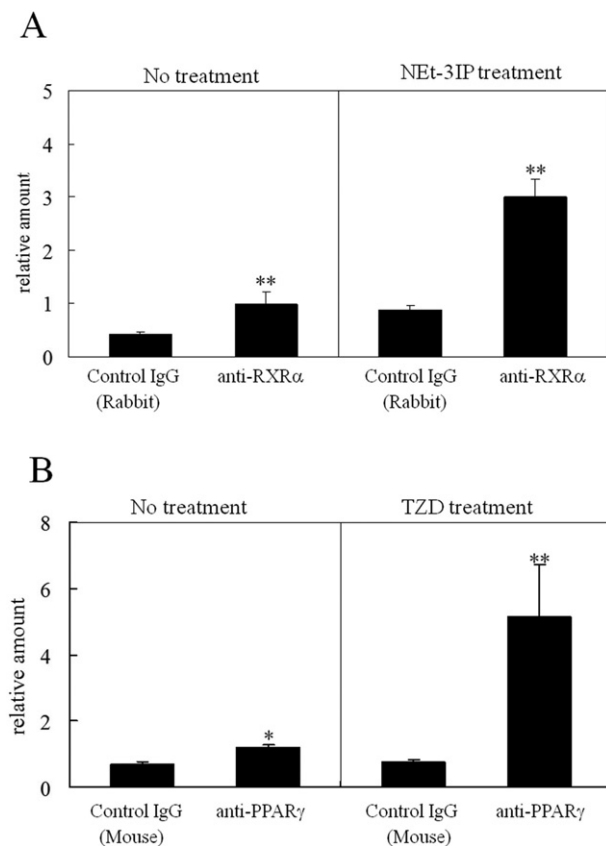


Fig. 6. Chromatin immunoprecipitation analysis of RXR α or PPAR γ binding to DR1/PPRE. Cross-linked chromatin complexes from NET-3IP-treated, TZD-treated or non-treated HOZOT cells were immunoprecipitated with anti-RXR α , anti-PPAR γ or control IgG. ChIP-qPCR was performed using primers described in Fig. 5. Relative amounts of the PCR product were normalized for those of corresponding input chromatin, and their relative precipitation was expressed as fold precipitation above the baseline. The values are shown as the means \pm SD. Data are representative results of three independent experiments. * $p < 0.01$ compared with the values of control IgG.

activities in regulating lipid and glucose metabolism, and also negatively modulating inflammation [28,29]. Anti-inflammatory roles of these two NRs have been shown in conditional KO mice. *Rxra* KO mice displayed elevated tumor necrosis factor- α and IFN- γ expression [23], whereas PPAR γ KO mice exhibited elevated inducible nitric oxide synthase and IFN- γ expression [29].

By *in vitro* functional studies, we demonstrated that both RXR α and PPAR γ agonistic ligands have inhibitory effects on IFN- γ production by HOZOTs. PPAR γ agonistic ligands exert inhibitory effects on cytokine production by T cells through various mechanisms, including inhibition of T cell activation, inhibited production of IL-2, induction of apoptosis, inhibition of IL-12 production by antigen presenting cell, or reduced IFN- γ production due to suppressed activation of c-Jun [28,30–32]. In our system, it is interesting that either RXR α or PPAR γ ligand independently but not synergistically inhibited IFN- γ production by HOZOTs (data not shown). To the best of our knowledge, we demonstrated for the first time that these inhibitory effects were mediated through direct binding of these two NRs to the IFN- γ promoter.

As previously discussed, RXR acts as both a homodimer as well as a heterodimer with PPAR γ . Therefore, the next question is where and how these dimers associate with DNA to control IFN- γ transcription in HOZOT. The RXR homodimer interacts with a specific sequence, the DR-1 element that is found on a variety of promoters or enhancers of several distinct genes such as rat cellular retinol-binding protein type II, human apo-A-I, human apo-A-II, and rat growth hormone [25].

Interestingly, the DR-1 element is also located in the IFN- γ promoter region. Therefore, one possibility is that NET-3IP exerts its inhibitory effects on IFN- γ production by forcing RXR homodimer to bind to IFN- γ 's DR-1 element. Another possibility is that RXR α heterodimer binds to DNA and exerts its inhibitory effects, a phenomenon known as a permissive effect. In this case, heterodimer partners could be PPAR γ or other NRs.

5. Conclusions

In conclusion, we found that RXR α and PPAR γ were selectively expressed in HOZOTs and can be used as signature NRs. We also demonstrated that RXR α and PPAR γ were functionally involved in cytokine production in HOZOT cells. Furthermore, both NRs repressed IFN- γ gene expression via binding to the PPRE/DR1 element in HOZOT cells. Our studies suggest a potential role for RXR α in the regulation of inflammation and might provide a pharmacological approach to modulating RXR α signaling as part of an overall strategy to suppress inflammation. Recently, Kakuta et al. [18] reported that type 2 diabetes was controlled *in vivo* by a treatment of NET-3IP. Their observation supports the speculation of our study.

Supplementary material

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.rinim.2012.08.001.

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